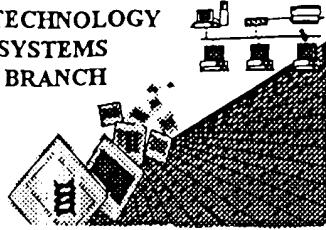


BIOTECHNOLOGY  
SYSTEMS  
BRANCH

01/20  
04/24



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/039,119  
Source: OIPC  
Date Processed by STIC: 4/17/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

**Raw Sequence Listing Error Summary**

**ERROR DETECTED**      **SUGGESTED CORRECTION**      **SERIAL NUMBER:** 111111

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1  Wrapped Nucleic  
       Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  Misaligned Amino  
       Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length      Sequence(s)  contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6  PatentIn 2.0  
       "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7  Skipped Sequences  
       (OLD RULES)      Sequence(s)  missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8  Skipped Sequences  
       (NEW RULES)      Sequence(s)  missing. If Intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
       (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213>  
       Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11  Use of <220>  
            Sequence(s) 4  missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
       "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n  
            n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



100% Comply  
OIPR  
Title Needed  
100% 1245

OIPR

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/039,119

DATE: 04/17/2002  
TIME: 14:12:50

Input Set : A:\STEM1110-4.ST25.txt  
Output Set: N:\CRF3\04172002\J039119.raw

2 <110> APPLICANT: STEM CELL PHARMACEUTICALS, INC.  
3 TWARDZIK, Daniel R.  
4 FELKER, Thomas S.  
5 PERNET, Andre  
6 PASKELL, Stefan  
8 <120> TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF  
USE THEREFOR  
10 <130> FILE REFERENCE: STEM1110-4  
12 <140> CURRENT APPLICATION NUMBER: US 10/039,119  
13 <141> CURRENT FILING DATE: 2002-01-04  
15 <150> PRIOR APPLICATION NUMBER: US 09/641,587  
16 <151> PRIOR FILING DATE: 2000-08-17  
18 <150> PRIOR APPLICATION NUMBER: US 09/492,935  
19 <151> PRIOR FILING DATE: 2000-01-27  
21 <150> PRIOR APPLICATION NUMBER: US 09/387,567  
22 <151> PRIOR FILING DATE: 1999-08-19  
24 <160> NUMBER OF SEQ ID NOS: 7  
26 <170> SOFTWARE: PatentIn version 3.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 50  
30 <212> TYPE: PRT  
31 <213> ORGANISM: Homo sapiens  
33 <400> SEQUENCE: 1  
35 Val Val Ser His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys  
36 1 5 10 15  
38 Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys  
39 20 25 30  
41 Val Cys His Ser Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu  
42 35 40 45  
44 Leu Ala  
45 50  
47 <210> SEQ ID NO: 2  
48 <211> LENGTH: 50  
49 <212> TYPE: PRT  
50 <213> ORGANISM: Rattus norvegicus  
52 <400> SEQUENCE: 2  
54 Val Val Ser His Phe Asn Lys Cys Pro Asp Ser His Thr Gln Tyr Cys  
55 1 5 10 15  
57 Phe His Gly Thr Cys Arg Phe Leu Val Gln Glu Lys Pro Ala Cys  
58 20 25 30  
60 Val Cys His Ser Gly Tyr Val Gly Val Arg Cys Glu His Ala Asp Leu  
61 35 40 45  
63 Asp Ala  
64 50

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/039,119

DATE: 04/17/2002  
TIME: 14:12:50

Input Set : A:\STEM1110-4.ST25.txt  
Output Set: N:\CRF3\04172002\J039119.raw

66 <210> SEQ ID NO: 3  
67 <211> LENGTH: 57  
68 <212> TYPE: PRT  
69 <213> ORGANISM: Artificial sequence  
71 <220> FEATURE:  
72 <223> OTHER INFORMATION: A modified human TGF-alpha sequence  
74 <400> SEQUENCE: 3  
76 Ser Leu Ser Leu Pro Ala Met Val Val Ser His Phe Asn Asp Cys Pro  
77 1 5 10 15  
79 Asp Ser His Thr Gln Phe Cys Phe His Gly Thr Cys Arg Phe Leu Val  
80 20 25 30  
82 Gln Glu Asp Lys Pro Ala Cys Val Cys His Ser Gly Tyr Val Gly Ala  
83 35 40 45  
85 Arg Cys Glu His Ala Asp Leu Leu Ala  
86 50 55  
88 <210> SEQ ID NO: 4  
89 <211> LENGTH: 11  
90 <212> TYPE: PRT  
91 <213> ORGANISM: Artificial sequence  
93 <220> FEATURE:  
94 <223> OTHER INFORMATION: Artificial peptide sequence  
96 <220> FEATURE:  
97 <221> NAME/KEY: VARIANT  
98 <222> LOCATION: (1)..(10)  
99 <223> OTHER INFORMATION: Xaa at residue 1, 5, 7 to 9 is independently V, G or A; Xaa  
at  
100 residue 6 is Y or F; and Xaa at residue 10 is R or K  
102 <400> SEQUENCE: 4  
W--> 104 Xaa Cys His Ser Xaa Xaa Xaa Xaa Xaa Cys  
105 1 5 10  
107 <210> SEQ ID NO: 5  
108 <211> LENGTH: 7  
109 <212> TYPE: PRT  
110 <213> ORGANISM: Artificial sequence  
112 <220> FEATURE:  
113 <223> OTHER INFORMATION: Artificial peptide sequence  
115 <220> FEATURE:  
116 <221> NAME/KEY: VARIANT  
117 <222> LOCATION: (1)..(7)  
118 <223> OTHER INFORMATION: Xaa at residue 1 and 4 is E or D; Xaa at residue 3 and 7 is  
V, G,  
119 or A; Xaa at residue 5 is L or I; and Xaa at residue 6 is D or E  
122 <400> SEQUENCE: 5  
W--> 124 Xaa His Xaa Xaa Xaa Xaa Xaa  
125 1 5  
127 <210> SEQ ID NO: 6  
128 <211> LENGTH: 18  
129 <212> TYPE: PRT  
130 <213> ORGANISM: Artificial sequence  
132 <220> FEATURE:  
133 <223> OTHER INFORMATION: Artificial peptide sequence

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/039,119

DATE: 04/17/2002  
TIME: 14:12:50

Input Set : A:\STEM1110-4.ST25.txt  
Output Set: N:\CRF3\04172002\J039119.raw

135 <220> FEATURE:  
136 <221> NAME/KEY: VARIANT  
137 <222> LOCATION: (1)..(18)  
138 <223> OTHER INFORMATION: Xaa at residue 1, 5, 7-9, 14, 18 is indep. V, G, or A; Xaa  
at  
139 residue 6 is Y or F; Xaa at residue 10 is R or K; Xaa at residue 12,  
140 15 is indep. E or D; Xaa at residue 16 is L or I; Xaa at residue  
141 17 is D or E  
143 <400> SEQUENCE: 6  
W--> 145 Xaa Cys His Ser Xaa Xaa Xaa Xaa Xaa Cys Xaa His Xaa Xaa Xaa  
146 1 5 10 15  
W--> 148 Xaa Xaa  
151 <210> SEQ ID NO: 7  
152 <211> LENGTH: 7  
153 <212> TYPE: PRT  
154 <213> ORGANISM: Artificial sequence  
156 <220> FEATURE:  
157 <223> OTHER INFORMATION: Artificial peptide sequence  
159 <220> FEATURE:  
160 <221> NAME/KEY: VARIANT  
161 <222> LOCATION: (1)..(7)  
162 <223> OTHER INFORMATION: Xaa at residue 1 and 2 is indep. V, G, and A; Xaa at residue  
7 is  
163 K or D  
165 <400> SEQUENCE: 7  
W--> 167 Xaa Xaa Ser His Phe Asn Xaa  
168 1 5

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/039,119

DATE: 04/17/2002

TIME: 14:12:51

Input Set : A:\STEM1110-4.ST25.txt

Output Set: N:\CRF3\04172002\J039119.raw

L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7